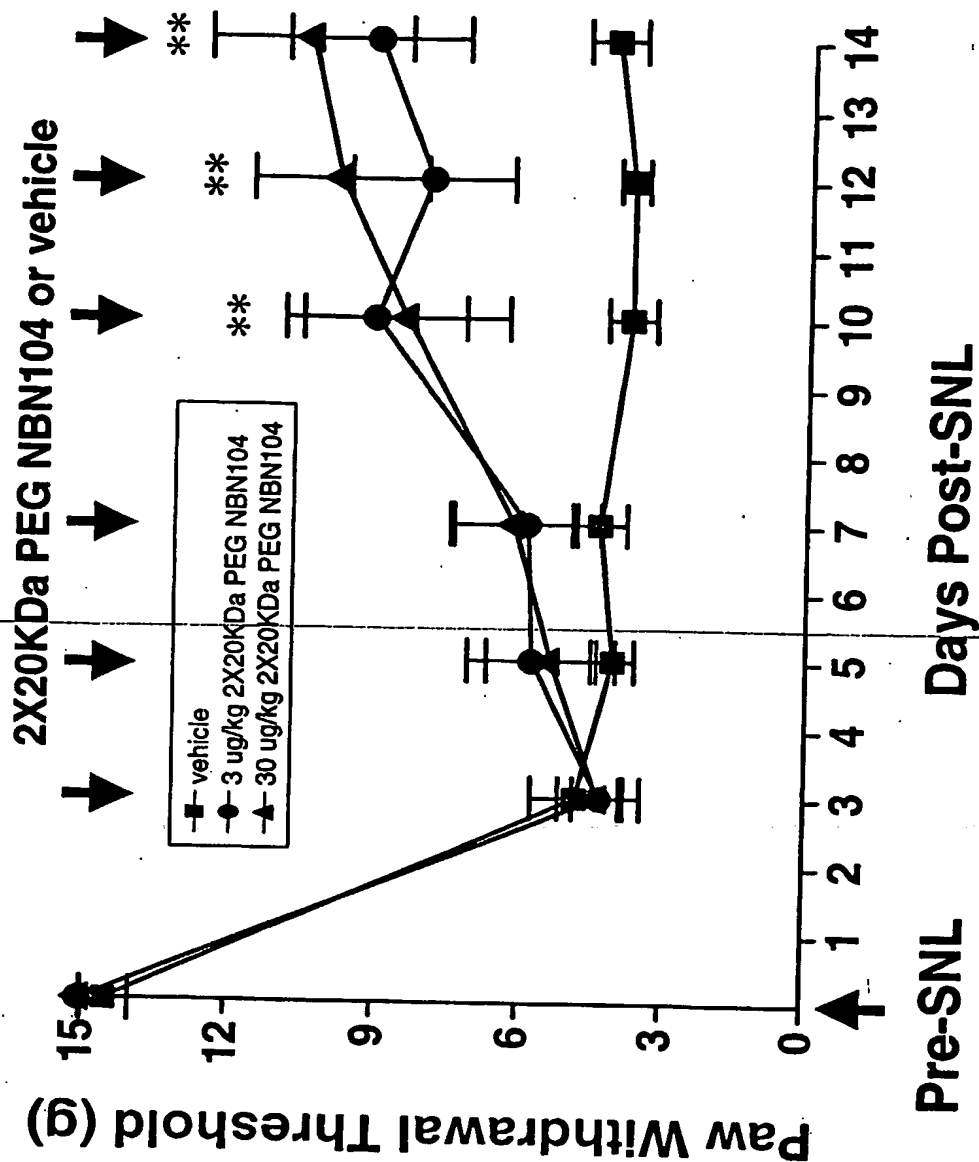


Figure 1

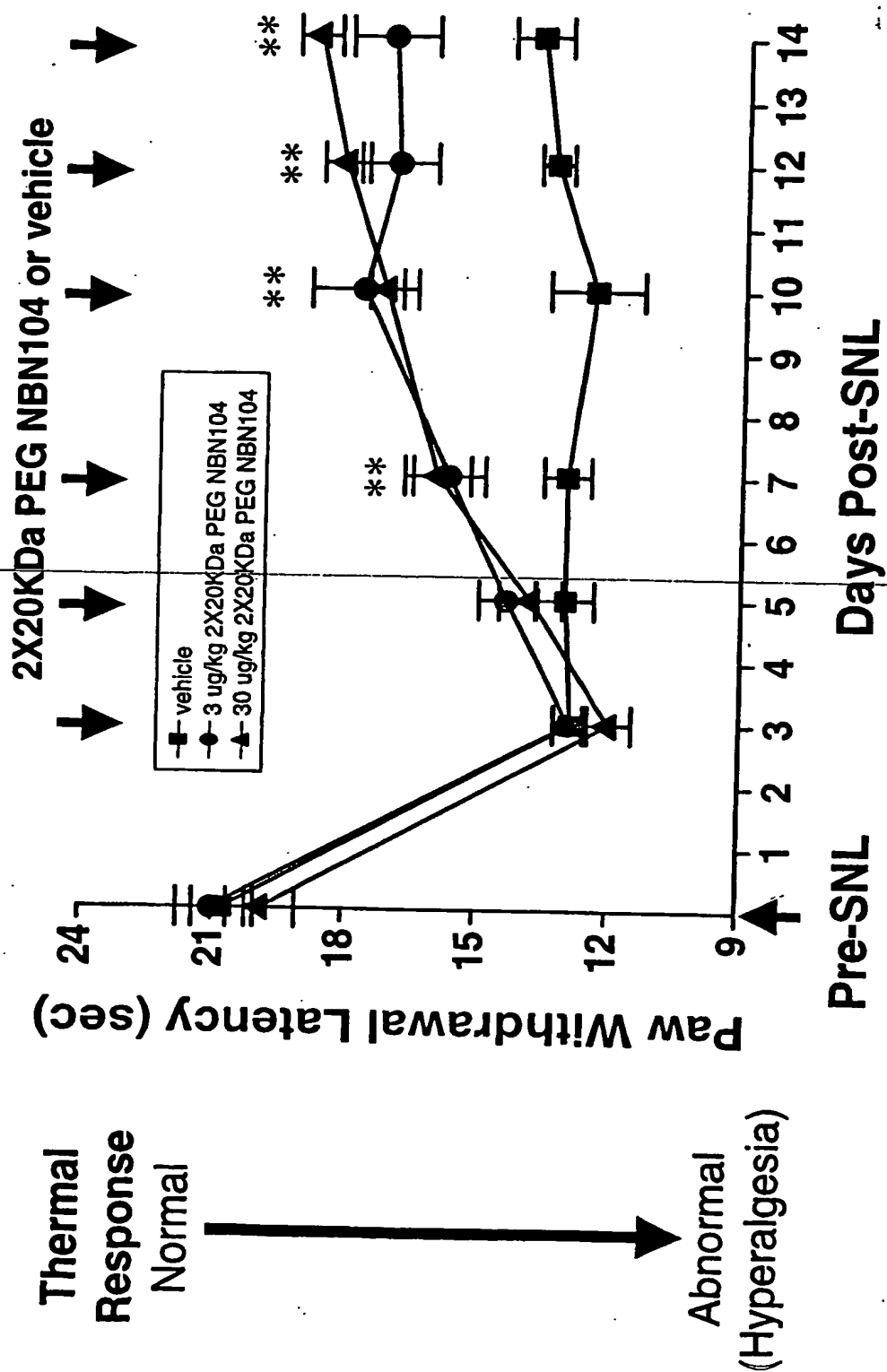


* p < 0.05 vs veh (2 Way RM ANOVA; SNK)

Tactile Response Normal

Abnormal (Allodynia)

Figure 2



* p < 0.05 vs veh (2 Way RM ANOVA; SNK)

FIG. 3

1	AGGPGSRARAAGARGCRLRSQVLPVRAIGLGHRSDELVRF	human
	AGTRSSRARTTDARGCRLRSQVLPVSALGLGHSSDELIRF	mouse
	AGTRSSRARATDARGCRLRSQVLPVSALGLGHSSDELIRF	rat
	ag---srar---argcrlrsqvpv-alglgh-sdel-rf	consensus
41	RFCSGSCRRARSPHDLSLASLLGAGALRPPPGSRPVSQPC	human
	RFCSGSCRRARSQHDLASLLGAGALRSPPGSRPISQPC	mouse
	RFCSGSCRRARSPHDLSLASLLGAGALRSPPGSRPISQPC	rat
	rfcsgscrrars-hdlsasllgagalr-ppgsrp-sqpc	consensus
81	CRPTRYEAVSFMDVNSTWRTVDRLSATAACGLG	human (SEQ ID NO:2)
	CRPTRYEAVSFMDVNSTWRTVDHLSATAACGLG	mouse (SEQ ID NO:3)
	CRPTRYEAVSFMDVNSTWRTVDHLSATAACGLG	rat (SEQ ID NO:4)
	crptryeavsfmdvnstwrtd-lsatacgclg	consensus (SEQ ID NO:1)
	*	* = Asn95

FIG. 4

Consensus sequence: (SEQ ID NO:1)

Ala Gly Xaa1 Xaa2 Xaa3 Ser Arg Ala Arg Xaa4 Xaa5 Xaa6 Ala Arg Gly Cys
 Arg Leu Arg Ser Gln Leu Val Pro Val Xaa7 Ala Leu Gly Leu Gly His Xaa8 Ser
 Asp Glu Leu Xaa9 Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg
 Ser Xaa10 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg
 Xaa11 Pro Pro Gly Ser Arg Pro Xaa12 Ser Gln Pro Cys Cys Arg Pro Thr Arg
 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp
 Xaa13 Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly

wherein:

Xaa ₁ is Gly or Thr	Xaa ₆ is Gly or Asp	Xaa ₁₁ is Pro or Ser
Xaa ₂ is Pro or Arg	Xaa ₇ is Arg or Ser	Xaa ₁₂ is Val or Ile
Xaa ₃ is Gly or Ser	Xaa ₈ is Arg or Ser	Xaa ₁₃ is Arg or His
Xaa ₄ is Ala or Thr	Xaa ₉ is Val or Ile	
Xaa ₅ is Ala or Thr	Xaa ₁₀ is Pro or Gln	

[illegible]

FIG. 6

	10	20	30	40	50	
NBN113	AGGPGSRARAAGARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN112	GGPGSRARAAGARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN111	GPGRARAAGARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN110	PGSRARAAGARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN109	GSRARAAGARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN108	SRARAAGARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN107	RARAAGARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN106	ARAAGARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN105	RAAGARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN104	AAGARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN103	AGARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN102	GARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN101	ARGCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN100	RCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR
NBN99	GCRLRSQ	LV	PVRALGLGHR	SD	ELVRFRC	SGSCRR

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	60	70	80	90	100	
NBN113	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	100
NBN112	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	99
NBN111	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	98
NBN110	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	97
NBN109	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	96
NBN108	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	95
NBN107	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	94
NBN106	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	93
NBN105	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	92
NBN104	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	91
NBN103	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	90
NBN102	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	89
NBN101	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	88
NBN100	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	87
NBN99	RSPHDL	SLASLLGAGALRPP	PGSRPVSQ	PCCRPT	RYEAVSFMDVNSTWRT	86

*

	110	
NBN113	VDRLS	SATACGCLG 113 (SEQ ID NO:2)
NBN112	VDRLS	SATACGCLG 112 (SEQ ID NO:8)
NBN111	VDRLS	SATACGCLG 111 (SEQ ID NO:9)
NBN110	VDRLS	SATACGCLG 110 (SEQ ID NO:10)
NBN109	VDRLS	SATACGCLG 109 (SEQ ID NO:11)
NBN108	VDRLS	SATACGCLG 108 (SEQ ID NO:12)
NBN107	VDRLS	SATACGCLG 107 (SEQ ID NO:13)
NBN106	VDRLS	SATACGCLG 106 (SEQ ID NO:14)
NBN105	VDRLS	SATACGCLG 105 (SEQ ID NO:15)
NBN104	VDRLS	SATACGCLG 104 (SEQ ID NO:16)
NBN103	VDRLS	SATACGCLG 103 (SEQ ID NO:17)
NBN102	VDRLS	SATACGCLG 102 (SEQ ID NO:18)
NBN101	VDRLS	SATACGCLG 101 (SEQ ID NO:19)
NBN100	VDRLS	SATACGCLG 100 (SEQ ID NO:20)
NBN99	VDRLS	SATACGCLG 99 (SEQ ID NO:21)

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